WHAT IS CLAIMED IS:

1. A method of screening for the presence of chromosomal alterations associated with cancer in a sample, the method comprising:

contacting a nucleic acid sample from a human patient with a probe which binds selectively to a target nucleic acid sequence at 3q26.3, wherein the probe is contacted with the sample under conditions in which the probe binds selectively with the target nucleic acid sequence to form a stable hybridization complex; and

detecting the formation of a hybridization complex.

2. The method of claim 1, wherein the target nucleic acid sequence is in a PIK3CA gene.

3. The method of claim 1, wherein the target nucleic acid sequence is in a GLUT2 gene.

4. The method of claim 1, wherein the nucleic acid sample is from a ovarian sample from the patient.

5. The method of claim 1, wherein the probe selectively hybridizes to a region between markers D3S1275 and D3S1548.

6. The method of claim 1, wherein the probe selectively hybridizes to the same nucleic acid sequence as a YAC clone having coordinates 806D8 or 945H6 in the Genethon/CEPH mega YAC library.

7. The method of claim 1, wherein the probe is a member of an array.

8. The method of claim 1, further comprising contacting the sample with a reference probe which binds selectively to a centromeric DNA.

9. The method of claim 1, wherein the step of detecting the hybridization complex comprises determining the copy number of the target sequence.

10. The method of claim 1, wherein the probe is labeled with digoxigenin or biotin.

11. The method of claim 1, wherein the step of detecting the hybridization complex is carried out by detecting a fluorescent label.

12. The method of claim 11, wherein the fluorescent label is FITC.

13. The method of claim 1, wherein the sample comprises a metaphase cell.

14. The method of claim 1, further comprising the step of contacting the sample with a probe which binds selectively to a target nucleic acid sequence at 19q13.1-19q13.2.

15. The method of claim 14, wherein the target nucleic acid sequence is in an AKT2 gene.

16. A kit for the detection of a chromosome alterations correlated with cancer, the kit comprising a compartment which contains a nucleic acid probe which binds selectively to a target nucleic acid sequence in 3q26, wherein the probe binds selectively with the target nucleic acid sequence.

17. The kit of claim 16, wherein the probe is labeled.

18. The kit of claim 17, wherein label is selected from the group consisting of digoxigenin and biotin.

19. The kit of claim 16, wherein the probe comprises a sequence from a PIK3CA gene.

20. The kit of claim 16, wherein the probe comprises a sequence from a GLUT2 gene.

21. The kit of claim 16, wherein the probe selectively hybridizes to a region between markers D3S1275 and D3S1548.

22. The kit of claim 16, wherein the probe selectively hybridizes to the same nucleic acid sequence as a YAC clone having coordinates 806D8 or 945H6 in the Genethon/CEPH mega YAC library.

23. A method of screening for the presence of chromosomal alterations associated with cancer in a sample, the method comprising:

contacting the sample with an antibody specifically immunoreactive with a protein antigen encoded by a nucleic acid sequence at 3q26.3; and

detecting the formation of an antigen/antibody complex.

24. The method of claim 23, wherein the nucleic acid sequence is a PIK3CA gene.

25. The method of claim 23, wherein the nucleic acid sequence is a GLUT2 gene.

26. The method of claim 23, wherein the sample is a serum sample from the patient.

27. The method of claim 23, wherein the step of detecting the antigen/antibody complex is carried out by detecting a fluorescent label.

28. A kit for the detection of chromosomal alterations associated with cancer, the kit comprising a compartment which contains an antibody which is specifically immunoreactive with a protein antigen encoded by a nucleic acid sequence at 3q26.

29. The kit of claim 28, wherein the nucleic acid sequence is a PIK3CA gene.

30. The kit of claim 28, wherein the nucleic acid sequence is a GLUT2 gene.

31. The kit of claim 28, wherein the antibody is labeled.

32. A method of inhibiting the pathological proliferation of cancer cells, the method comprising inhibiting the activity of a gene product of an endogenous gene at 3q26.3.

33. The method of claim 32, wherein the endogenous gene maps to a region between markers D3S1275 and D3S1548.

34. The method of claim 32, wherein the endogenous gene maps to a region defined by YACs having coordinates 806D8 and 945H6 in the Genethon/CEPH mega YAC library.

35. The method of claim 32, wherein the endogenous gene is PIK3CA.

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